

Figure 1A

1 CCCACGCGTCCGATTAAAGTGAGGAGAGAGCTACAACCAAGTAAGCAAGTGTGTCAGGGGCTC 60
 61 ACCRACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCAA 120
 1 M Q G Q G R R R G T C K D I F C S K 18
 121 AATGGCATCTTACCTTTATGGAGTACTCTTTGCTGTGGCCTCTGTGCTCCAATCTACTG 180
 19 M A S Y L Y G V L F A V G L C A P I Y C 38
 181 TGTGTCCCCGGCCAATGCCCCAGTGCATACCCCCGCCCTTCCCTCCACAAAGAGCACCCC 240
 39 V S P A N A P S A Y P R P S S T K S T P 58
 241 TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGT 300
 59 A S Q V Y S L N T D F A F R L Y R R L V 78
 301 TTTGGAGACCCCGAGTCAGAACATCTTCTTCTCCCCCTGTGAGTGTCTCCACTTCCCTGGC 360
 79 L E T P S Q N I F F S P V S V S T S L A 98
 361 CATGCTCTCCCTTGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCCTGGGCTT 420
 99 M L S L G A H S V T K T Q I L Q G L G F 118
 421 CAACCTCACACACACACCAGAGTCTGCCATCCACAGGGCTTCCAGCACCCTGGTTCACTC 480
 119 N L T H T P E S A I H Q G F Q H L V H S 138
 481 ACTGACTGTCTCCAGCAAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTCGTCAAGAA 540
 139 L T V P S K D L T L K M G S A L F V K K 158
 541 GGAGCTGCAGCTGCAGGCAAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGT 600
 159 E L Q L Q A N F L G N V K R L Y E A E V 178
 601 CTTTCTACAGATTCTCCAACCCCTCCATTGCCAGGCGAGGATCAACAGCCATGTGAA 660
 179 F S T D F S N P S I A Q A R I N S H V K 198
 661 AAAGAAGACCCAAGGGAAGGTTGTAGACATAATCCAAGGCCTTGACCTTCTGACGCCAT 720
 199 K K T Q G K V V D I I Q G L D L L T A M 218
 721 GGTCTGGTGAATCACATTTTCTTTAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATA 780
 219 V L V N H I F F K A K W E K P F H L E Y 238
 781 TACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT 840
 239 T R K N F P F L V G E Q V T V Q V P M M 258
 841 GCACCAGAAAGAGCAGTTCGCTTTTGGGGTGGATACAGAGCTGAACTGCTTTGTGTGCA 900
 259 H Q K E Q F A F G V D T E L N C F V L Q 278

Figure 2

1 50
 AL132708_FL (1) MQGQRRRGTCCKDIFCSKMASYLYGVLFPAVGLCAPIYCVSPANAPSAYPR
 AACT_HUMAN (1) -----MERMLPLALGLLEAGFCPAVLCHPNPLD
 KAIN_HUMAN (1) -----MHLIDYLLLLVLVSLLSHQQQLHVHDEGSCS
 THBG_HUMAN (1) -----MSPFLYLVLLVLSLHATHICASPGEKVTACHS

51 100
 AL132708_FL (51) PS-----STKSTPASQVYSNLTPAFRLVRRVLVETFSQNIFFSPVSV
 AACT_HUMAN (51) EENLTQENQDRGTHVDLGLASAVDFRSLQKQLVLKAPDKNVISFSPSI
 KAIN_HUMAN (33) NSSHQILETGEQSPSLKIAPADAFPRFYLIASPTGKNYIFSPSLSI
 THBG_HUMAN (33) -----SQPNATLYKMSSINADPAFNLVRRFTVETEDKNIFFSPVSI

101 150
 AL132708_FL (94) STSLAMESLGAHSVTKTQFLQGLGFNTHTPESAIHQCFCHLVHSTITVPS
 AACT_HUMAN (81) STALAFSLGAHNNTLTETLKGGLKPNITETSEAEIHQSFCHELLRTINQSS
 KAIN_HUMAN (83) SAAYAMSLGACSHSRSSQLLEGGENTELSESDDVHRGEOHLLHTNLPG
 THBG_HUMAN (74) SAALVMTSFGACCSQTETVETLGTPLDTPMVEIQHGFHLLCSINPFK

151 200
 AL132708_FL (144) KDTLKMSSALFVKKEQLQANLGNVKRLVEAEVSTDSNPSIAQARI
 AACT_HUMAN (131) DEQLSMENAMFVKEQSLSDRPTEDAKRLGSEAPAMDEQDSAAAKKL
 KAIN_HUMAN (133) HGETRVSSALSLSHNFKFLAKFLNDTMAVVEAKLHUNNEYDVTGTIQL
 THBG_HUMAN (124) KELQLQINSLLEIGKHLKPLAKFLNDVKTLMEVETSDSNISAAQKE

201 250
 AL132708_FL (194) NSHVKKKTCGVVDVITQGLDLLTAMVLVNHFFPKAKWEKPEHLEYERKNF
 AACT_HUMAN (181) NDYVKNCRFGKITDLIKDSDGTMMVLVNYFFPKAKWEMPDPQDTHQR
 KAIN_HUMAN (183) NDHVKKETGRKIVDLVSEPKKDVLMVNVYFFPKLWKEKRISSRTPKD
 THBG_HUMAN (174) NSHVEMOKKGVVGLIQDKPNTINVLVNYFFPKAKWEMPDPQDTHQR

251 300
 AL132708_FL (244) PFLVGEQVTVQVPMHMQKEQFAFGVITEINCFVLQMDVKGDAVAFEVPS
 AACT_HUMAN (231) FYLSKKKQWVMPMMSLHHLTIYPYPRDEESSCTVVELKKTGNASALFIID
 KAIN_HUMAN (233) FYVDENTTVRVPMMLQDQEHHWYLDHRYTPCSMLRMDVKGDAVTFVFIEN
 THBG_HUMAN (224) SPLDKTTTVQVPMHMQEQYYHLVMEINCFVLQMDVSKNALALEVLEK

301 350
 AL132708_FL (294) KGKMRQLGALSARTLTKVSHSTQKR---WIEVPIERSTASINDETI
 AACT_HUMAN (281) QDKMEVEEAMLLPETIKRRRDSLEFR---EIGELYLPKEKIGRRDYNNDI
 KAIN_HUMAN (283) QGKREITEVLTPEMIMRNNLLRKNRNFYKYLEHLIKKSTSGSVLDQI
 THBG_HUMAN (274) EGQVESVGAAMSSKTEKKLNRLQKG---WVDLVFKKSTISATIDGAT

351 400
 AL132708_FL (340) LPKMGIQNAFDKNADFSLAKRDSQVSKATHKAVLDVSEEGIEATATT
 AACT_HUMAN (328) LQLGIEEAFSTKEDLSGITGARNLAVSQVVRKAVLDVDFEGIEGSHATA
 KAIN_HUMAN (333) LPRLEGTDLFSKWADLSGITKQQLKASKSFHATLDVDEASTEAATAT
 THBG_HUMAN (320) LKMGIQHAYSENADFSLTEDNGEKLNAAKAVLHIGKQKTESAAVPE

401 446
 AL132708_FL (390) TKFIVRSKDGPSYFTVSPNRTFLMMATNKAIDGILLGKLENPTKS
 AACT_HUMAN (378) VKITLLSALVETRITVFRNRPFLMIIVPTDQNIFFMSKVITNEKQA
 KAIN_HUMAN (383) FAIKFFSAQTN-RHILRFNRPFLVVFSTSTQSVLELGLVVDVETPK
 THBG_HUMAN (370) VELSDQPENTFLHPITQIDSEMLLRLERSRSLILGLGVNTEA

Figure 3

LSI-01 MQQGRRRGRT CKDIFCSKMA SYLYGVLPFAV GLCAPIYCVS PANAPSAYFR
 pdb1qlp MDPQ GDAQKQTDTS

LSI-01 PSSTKSTPAS QVYSLNTDFA FRLYRRLVLE TFSQNIFFSF VSVSTSLANL
 pdb1qlp HHDQDHPTFN KITPNLAFA FSLYRQLAHQ SNSNIFFSF VSIATAFAMI

LSI-01 SLGAHSVTKT QTLQGLGNE HTTPESALHQ GFQHLVHSLT VESKDETLKM
 pdb1qlp SLGTTKADTHD ETLLEGNTNLL TEIPEAQINE GFQELLRTIN QPDSQQLQTT

LSI-01 GSAIVVKKEI QIQANFLGMY KRLYEAEVFS TDESNSIQA ARINSHVREK
 pdb1qlp GNGLFLSEGI KIVDKKLEDV KKLHSEAFI VNFQDTEAK KQINDYVEG

LSI-01 TQKVVYDIQ GLDLLAMVL VNIIFKAKW ERPEHLEYTR KNFPELVGEQ
 pdb1qlp TQKIVDLVK ELDRDTVFAL VNIIFKCKW ERPEVKDT. EEDDPHVDQV

LSI-01 VTVOVPMHQ KEQFAGVDT ELNCFWLQMD YKQDAVAFV LSKGEMRQI
 pdb1qlp TTUKVPMHK LGMFNIQCK KLSWYLLMK YLGNATAEF LEDEGKLQHL

LSI-01 EQALSARTLI KWSHSLQKW IEVFIERFSI SASYNLETIL PKMQLQAFD
 pdb1qlp ENELTHDIT FLENEDERS ASLHLKLSI TGTYDLKSVL GQLGTVKVS

LSI-01 KNADFSIAK RDSIQVSKAT HKAVLDVSEE GTEATATTT KPIVRSKDG
 pdb1qlp NGABLSVTE EAPKLSKAV HRAVLIDEK GTRACAMFL EAPMSI..P

LSI-01 S.YFTVSENR TELMMITKA EDGILELQKV ENPTKS
 pdb1qlp PE...VKENK PFVFLMIEQN TRSPLEMRV VNEPQK

Figure 4.

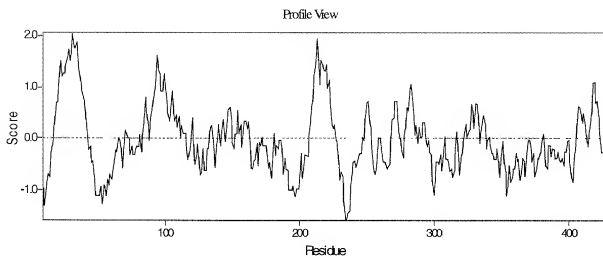


Figure 5.

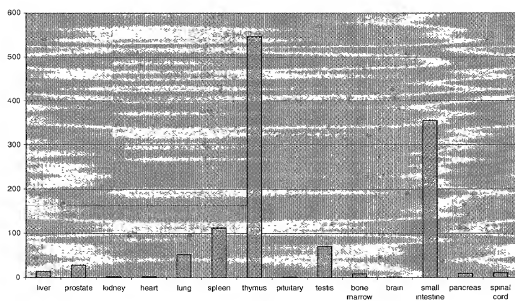
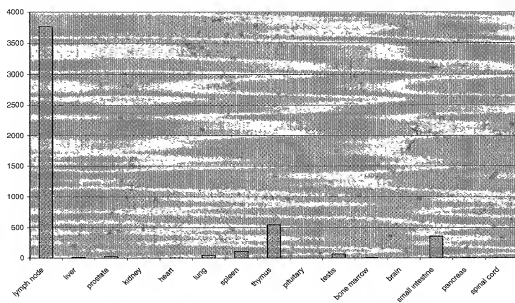


Figure 6.

Protein	Genbank ID	Identities	Similarities
human α_1 -antichymotrypsin	gi112874	46%	52%
human Kallistatin	gi5453888	48%	56%
human thyroxin-binding globulin	gi137142	51%	57%
human α_1 -antithrypsin	gi16137432	43%	50%

Figure 7

